

ained from fruits and from the hydrolysis of sucrose (milk sugar); galactose, obtained from the hydrolysis of lactose (milk sugar); and mannose, obtained from the digestion of polysaccharides and glycoproteins. After digestion, the monosaccharides enter the bloodstream, which carries them to various tissues. The metabolism of fructose, galactose, and mannose proceeds by their conversion to glycolytic intermediates, from which point they are broken down identically to glucose.

A. Fructose

Fructose is a major fuel source in diets that contain large amounts of sucrose (a disaccharide of fructose and glucose). There are two pathways for the metabolism of fructose; one occurs in muscle and the other occurs in liver. This dichotomy results from the different enzymes present in these various tissues.

Fructose metabolism in muscle differs little from that of glucose. Hexokinase (Section 16-2A), which converts glucose to G6P on entry into muscle cells, also phosphorylates fructose, yielding F6P (Fig. 16-34, left). The entry of fructose into glycolysis therefore involves only one reaction.

Liver contains little hexokinase; rather it contains glucokinase, which phosphorylates only glucose (Section 16-2A). Fructose metabolism in liver must therefore differ from that in muscle. In fact, liver converts fructose to glycolytic intermediates through a pathway that involves six enzymes (Fig. 16-34, right):

1. Fructokinase catalyzes the phosphorylation of fructose by ATP at C1 to form fructose-1-phosphate. Neither hexokinase nor phosphofructokinase can phosphorylate fructose-1-phosphate at C6 to form the glycolytic intermediate fructose-1,6-bisphosphate.

2. Class I aldolase (Section 16-2D) has several isoenzymic forms. Muscle contains Type A aldolase, which is specific for fructose-1,6-bisphosphate. Liver, however, contains Type B aldolase, which also utilizes fructose-1-phosphate as a substrate (Type B aldolase is sometimes called fructose-1-phosphate aldolase). In liver, fructose-1-phosphate therefore undergoes an aldol cleavage (Section 16-2D):



The glyceraldehyde thus formed is converted to glyceraldehyde-3-phosphate by Reaction 3, or to dihydroxyacetone phosphate by a combination of Reactions 4 to 6 (Fig. 16-34).

Direct phosphorylation of glyceraldehyde by ATP through the action of glyceraldehyde kinase forms the glycolytic intermediate glyceraldehyde-3-phosphate.

Alternatively, glyceraldehyde is converted to the glycolytic intermediate dihydroxyacetone phosphate by

reduction to glycerol by NAD⁺ as catalyzed by alcohol dehydrogenase (Reaction 4), phosphorylation to glycerol-3-phosphate by ATP through the action of glycerol kinase (Reaction 5), and reoxidation by NADH to dihydroxyacetone phosphate as mediated by glycerol phosphate dehydrogenase (Reaction 6).

As this complex series of reactions suggests, the liver has an enormous repertory of enzymes. This is because the liver is involved in the breakdown of a great variety of metabolites. Efficiency in metabolic processing dictates that many of these substances be converted to glycolytic intermediates. The liver, in fact, contains many of the enzymes necessary to do so.

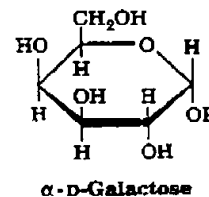
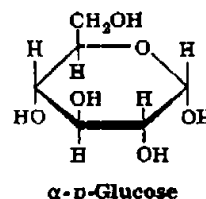
Excessive Fructose Depletes Liver P_i

At one time, fructose was thought to have advantages over glucose for intravenous feeding. The liver, however, encounters metabolic problems when the blood concentration of this sugar is too high (higher than can be attained by simply eating fructose-containing foods). When the fructose concentration is high, fructose-1-phosphate may be produced faster than Type B aldolase can cleave it. Intravenous feeding of large amounts of fructose may therefore result in high enough fructose-1-phosphate accumulation to severely deplete the liver's store of P_i. Under these conditions, [ATP] drops, thereby activating glycolysis and lactate production. The lactate concentration in the blood under such conditions can reach life-threatening levels.

Fructose intolerance, a genetic disease in which ingestion of fructose causes the same fructose-1-phosphate accumulation as with its intravenous feeding, results from a deficiency of Type B aldolase. This condition appears to be self-limiting: Individuals with fructose intolerance rapidly develop a strong distaste for anything sweet.

B. Galactose

Galactose comprises half of the milk sugar lactose, and is thus a major fuel constituent of dairy products. Galactose and glucose are epimers that differ only in their configuration about C4.



The enzymes of glycolysis are specific; they do not recognize the galactose configuration. An epimerization reaction must therefore be carried out before galactose enters the glycolytic pathway. This reaction takes place after the conversion of galactose to its uridine diphosphate derivative.

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The role of UDP-sugars and other nucleotidyl-sugars is discussed in more detail in Sections 17-2 and 21-3. The entire pathway converting galactose to a glycolytic intermediate involves four reactions (Fig. 16-35):

1. Galactose is phosphorylated at C1 by ATP in a reaction catalyzed by **galactokinase**.
2. **Galactose-1-phosphate uridylyl transferase** transfers the uridylyl group of UDP-glucose to galactose-1-phosphate to yield **glucose-1-phosphate (G1P)** and **UDP-galactose** by the reversible cleavage of UDP-glucose's pyrophosphoryl bond.
3. **UDP-galactose-4-epimerase** converts **UDP-galactose** back to **UDP-glucose**. This enzyme has an associated NAD^+ , which suggests that the reaction involves the

sequential oxidation and reduction of the hexose C4 atom:

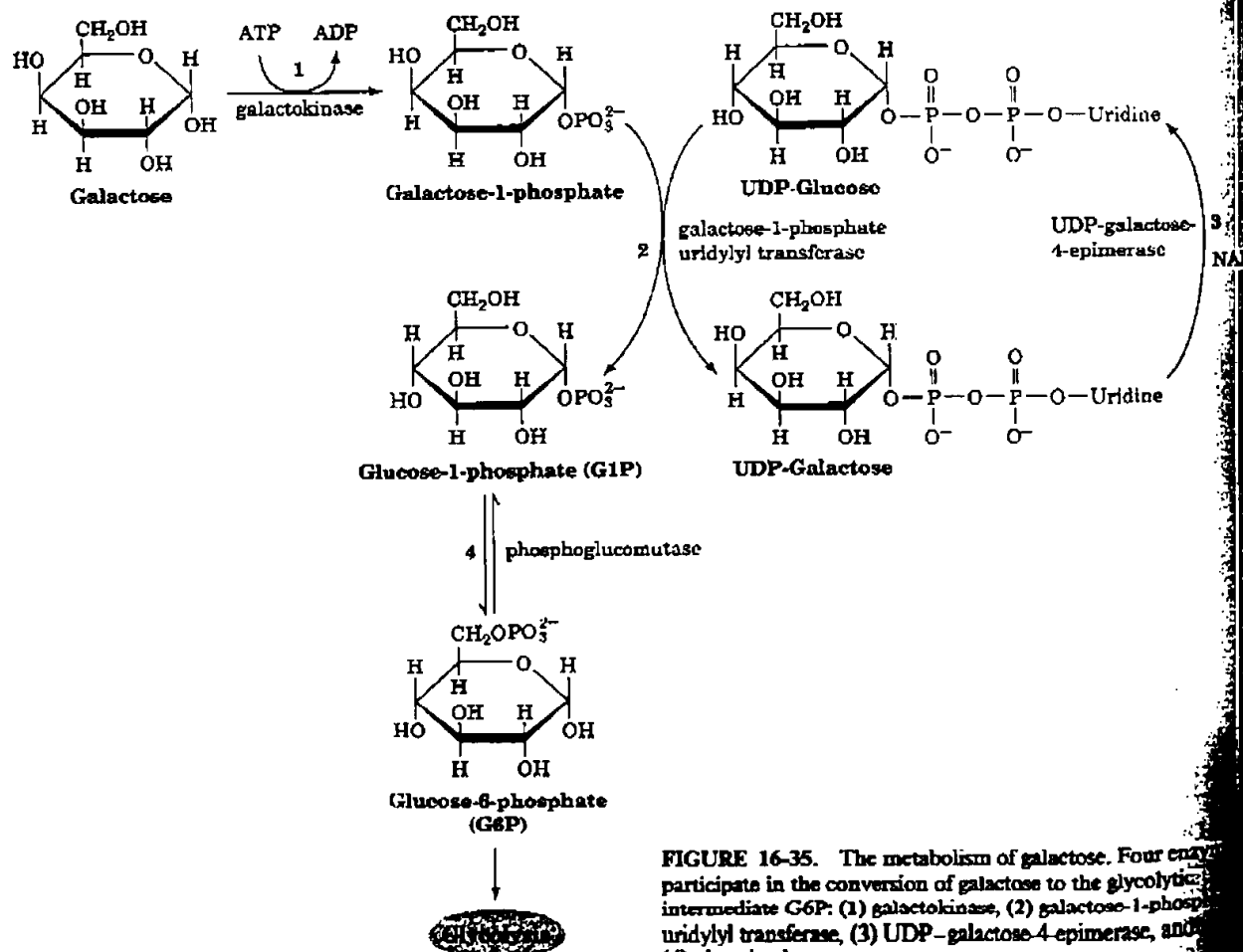
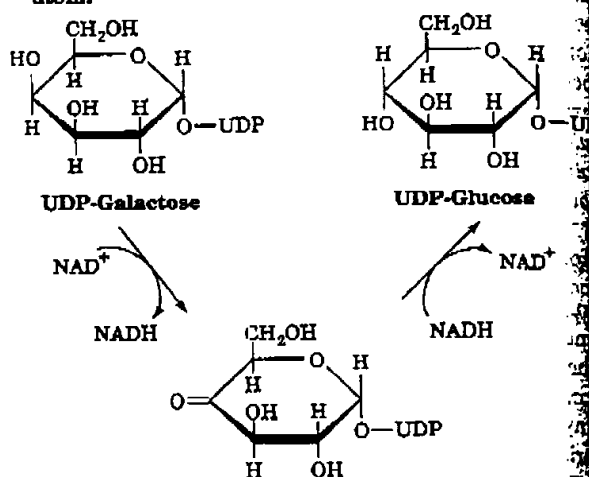


FIGURE 16-35. The metabolism of galactose. Four enzymes participate in the conversion of galactose to the glycolytic intermediate G6P: (1) galactokinase, (2) galactose-1-phosphate uridylyl transferase, (3) UDP-galactose-4-epimerase, and (4) phosphoglucomutase.

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Official Name	
UTP--hexose-1-phosphate uridylyltransferase.	
Alternative Name(s)	
Galactose-1-phosphate uridylyltransferase.	
Reaction catalysed	
UTP + alpha-D-galactose 1-phosphate <=> diphosphate + UDP-galactose	
Comments	
<ul style="list-style-type: none"> Alpha-D-glucose 1-phosphate can also act as acceptor, more slowly. 	
Human Generic Disease(s)	
Galactosemia	MIM:230400
Cross-references	
Biochemical Pathways; map number(s)	B4
PROSITE	PDOC00108
BRENDA	2.7.7.10
EMP/PUMA	2.7.7.10
WIT	2.7.7.10
KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE	2.7.7.10
IUBMB Enzyme Nomenclature	2.7.7.10
MEDLINE	Find literature relating to 2.7.7.10
Swiss-Prot	E40908, GAL7_CRYNE; P09148, GAL7_ECOLI; P31764, GAL7_HAEIN; P07902, GAL7_HUMAN; P09580, GAL7_KLULA; Q03249, GAL7_MOUSE; P43424, GAL7_RAT; P22714, GAL7_SALTY; Q9HD05, GAL7_SCHPO; P13212, GAL7_STRLI; C33836, GAL7_THEMA; P08431, GAL7_YEAST; Q9KDV2, GALT_BACHD; P39575, GALT_BACSU; P15981, GALT_BUTFI; Q97E24, GALT_CLOAB; Q8XKE3, GALT_CLOPE; Q8RHC9, GALT_FUSNN; Q84904, GALT_LACCA; Q00051, GALT_LACHE; Q9CE63, GALT_LACLA; Q9S693, GALT_LACLC; Q93MM1, GALT_LACSK; Q9RGR9, GALT_STACA; P96994, GALT_STRMU; Q8VS92, GALT_STRSL; Q9ZB09, GALT_STRTR; Q8R8R6, GALT_THETN; Q97P15, GAT1_STRFN; Q97N27, GAT2_STRPN;

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General information about the entry

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Primary accession number **P09148**
Secondary accession number **P78270**
Entered in Swiss-Prot in **Release 10, March 1989**
Sequence was last modified in **Release 35, November 1997**
Annotations were last modified in **Release 41, February 2003**
Name and origin of the protein
Protein name **Galactose-1-phosphate uridylyltransferase**
Synonym **EC 2.7.7.10**
Gene name **GALT or GALB or B0758**
From **Escherichia coli [TaxID: 562]**
Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.**

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Comments

- **CATALYTIC ACTIVITY:** UTP + alpha-D-galactose 1-phosphate = diphosphate + UDP-galactose.
- **PATHWAY:** Galactose metabolism; second step.
- **SUBUNIT:** Homodimer.
- **SIMILARITY:** BELONGS TO THE GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE FAMILY 1.

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AE000178; AAC73845.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
D90714; BAA35420.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
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PIR S00722; XNECUD.

PDB 1GUP; 12-NOV-97. [[ExPASy](#) / [RCSB](#)]
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1HXP; 08-NOV-96. [[ExPASy](#) / [RCSB](#)]
1HXQ; 22-OCT-97. [[ExPASy](#) / [RCSB](#)]
[Detailed list of linked structures.](#)

EcoGene EG10366; galT.

EcoCyc EG10366; galT.

CMR P09148; B0758.
[IPR001937](#); GalP_UDPtransf1.
[IPR005851](#); GalP_Utransf_1.

InterPro [IPR005850](#); GalP_Utransf_C.
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ProDom [PD005051](#); GalP_UDPtransf1; 1.
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PROSITE [PS00117](#); GAL_P_UDP_TRANSF_I; 1.

BLOCKS [P09148](#).

ProNet [P09148](#).

ProtoMap [P09148](#).

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Keywords

Transferase; Nucleotidyltransferase; Galactose metabolism; 3D-structure; Complete proteome.

Features



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Official Name	
Galactokinase.	
Alternative Name(s)	
None.	
Reaction catalysed	
ATP + D-galactose <=> ADP + D-galactose 1-phosphate	
Comments	
• D-galactosamine can also act as acceptor.	
Human Genetic Disease(s)	
Galactokinase deficiency	MIM:230200
Cross-references	
Biochemical Pathways; map number(s)	B4
PROSITE	PDOC00099, PDOC00545
BRENDA	2.7.1.6
EMP/PUMA	2.7.1.6
WIT	2.7.1.6
KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE	2.7.1.6
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MEDLINE	Find literature relating to 2.7.1.6
Swiss-Prot	P94169, GAL1_ACTPL; Q9SE55, GAL1_ARATH; Q9KDV4, GAL1_BACHD; P39574, GAL1_BACSU; P56091, GAL1_CANAL; P56599, GAL1_CANMA; Q42821, GAL1_CANPA; Q97E26, GAL1_CLOAB; Q8XKP9, GAL1_CLOPE; P06976, GAL1_ECOLI; Q8RH00, GAL1_FUSNN; P31767, GAL1_HAEIN; P51570, GAL1_HUMAN; P09608, GAL1_KLULA; Q84902, GAL1_LACCA; Q00052, GAL1_LACHE; Q9R7D7, GAL1_LACLA; Q9S692, GAL1_LACLC; Q9RON0, GAL1_MOUSE; P26910, GAL1_MYCTU; P57899, GAL1_PASMU; Q9HHB6, GAL1_PYRFU; Q58107, GAL1_PYRHO; Q8Z8B0, GAL1_SALT1; P22713, GAL1_SALTY; Q9H0U2, GAL1_SCHPO; Q9RG51, GAL1_STACA; Q9K358, GAL1_STRCO; P13227, GAL1_STRLI; P96923, GAL1_STRMU; Q97NZ6, GAL1_STRPN; Q92B10, GAL1_STRTR; P56838, GAL1_THEMA; Q85253, GAL1_THENE; Q8R8R7, GAL1_THETN; Q83433, GAL1_TREPA; Q9KRP1, GAL1_VIBCH; P04385, GAL1_YEAST; Q8ZGY3, GAL1_YERPE;

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General information about the entry

Entry name **GAL1_ECOLI**
 Primary accession number **P06976**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 07, April 1988
 Sequence was last modified in Release 10, March 1989
 Annotations were last modified in Release 41, February 2003
 Name and origin of the protein
 Protein name **Galactokinase**
 Synonyms **EC 2.7.1.6**
Galactose kinase
 Gene name **GALK or GALA or B0757 or Z0927 or ECS0785**
 From **Escherichia coli** [TaxID: 562]
Escherichia coli O157:H7 [TaxID: 83334]
 Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia**

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 "The complete genome sequence of Escherichia coli K-12."
 Science 277:1453-1474(1997).

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Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kubara S., Shiba T., Hattori M., Shinagawa H.;
 "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
 DNA Res. 8:11-22(2001).

[6] SEQUENCE OF 370-381 FROM NUCLEIC ACID.

MEDLINE=95055764; PubMed=7966338; [NCBI, ExPASy, EBI, Israel, Japan]

Bouffard G.G., Rudd K.E., Adhya S.L.;

"Dependence of lactose metabolism upon mutarotase encoded in the gal operon in Escherichia coli.";
 J. Mol. Biol. 244:269-278(1994).

[7] SEQUENCE OF 1-19.

MEDLINE=78043686; PubMed=200486; [NCBI, ExPASy, EBI, Israel, Japan]

Schlesinger D.H., Schell M.A., Wilson D.B.;

"The NH2-terminal sequences of galactokinase from Escherichia coli and Saccharomyces cerevisiae.";
 FEBS Lett. 83:45-47(1977).

Comments

- **CATALYTIC ACTIVITY:** ATP + D-galactose = ADP + D-galactose 1-phosphate.
- **PATHWAY:** Galactose metabolism; first step.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*Potential*).
- **SIMILARITY:** BELONGS TO THE GHMP KINASE FAMILY. GALK SUBFAMILY.

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Cross-references

EMBL	X02306; CAA26172.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AE000178; AAC73844.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] D90714; BAA35419.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AE005253; AAG55086.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AP002553; BAB34208.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] U13636; AAB17019.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	B23044; KIECGG. A13446; A13446.
EcoGene	EG10363; galk.
EcoCyc	EG10363; galk.
CMR	P06976; B0757.
HAMAP	MF_00246; -, 1. IPR000705; Galactokinase. IPR001174; Galkinase. IPR006204; GHMP_kinase. IPR006203; GHMPkinse_ATP. IPR006206; Mev_galkinase. Graphical view of domain structure.
Pfam	PF00288; GHMP_kinases; 1. PR00473; GALCTOKINASE.
PRINTS	PR00960; LMBPPROTEIN. PR00959; MEVGALKINASE.
TIGRFAMs	TIGR00131; gal_kin; 1.
PROSITE	PS00106; GALACTOKINASE; 1. PS00627; GHMP_KINASES_ATP; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	P06976.
ProtoNet	P06976.
ProtoMap	P06976.
PRESAGE	P06976.
DIP	P06976.
ModBase	P06976.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

Transferase; Kinase; Galactose metabolism; ATP-binding; Complete proteome.

Features



Feature table viewer

Key	From	To	Length	Description
INIT_MET	0	0		
NP_BIND	121	131	11	ATP (POTENTIAL).

Sequence information

Length: 381 AA Molecular weight: 41311 Da CRC64: E4902DF7747288BA [This is a checksum on the sequence]

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70	80	90	100	110	120
RKVRVMAADY	ENQLDEFSLD	APIVAHENYQ	WANYVRGVVK	HLQLRNNSFG	GVDMVISGNV
130	140	150	160	170	180
PQGAGLSSSA	SLEVAVGTVL	QQLYHLPLDG	AQIALNGQEA	ENQFVGNCNG	IMDQLISALG
190	200	210	220	230	240
KKDHALLIDC	RSLGTKAVSM	PKGVAVVIIN	SNFKRTL VGS	EYNTREQCE	TGARFFQQPA
250	260	270	280	290	300
LROVTIEEFN	AVARELDFIV	AKRVRHILTE	NARTVEAASA	LEQGD LKRMG	ELMAESHASM
310	320	330	340	350	360
RDDFEITVPQ	IDTLVEIVKA	VIGDKGGVRM	TGGGFGGCIV	ALIFEELVEA	VQQA VAEQYE
370	380				
AKTGIKETFY	VCKPSQGAGQ	C			

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Search for

NiceZyme View of ENZYME: EC 5.1.3.2

Official Name	
UDP-glucose 4-epimerase.	
Alternative Name(s)	
UDP-galactose 4-epimerase. Galactowaldenase. Uridine diphosphate galactose 4-epimerase. Uridine diphospho-galactose 4-epimerase.	
Reaction catalysed	
UDP-glucose <=> UDP-galactose	
Cofactor(s)	
NAD.	
Comments	
• Also acts on UDP-2-deoxyglucose.	
Human Genetic Disease(s)	
Galactose epimerase deficiency	MIM:230350
Cross-references	
Biochemical Pathways; map number(s)	B4, B5
BRENDA	5.1.3.2
EMP/PUMA	5.1.3.2
WIT	5.1.3.2
KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE	5.1.3.2
IUBMB Enzyme Nomenclature	5.1.3.2
MEDLINE	Find literature relating to 5.1.3.2
Swiss-Prot	Q59083, EXOB_AZOBR; Q59745, EXOB_RHIL; P26503, EXOB_RHME; Q42605, GAE1_ARATH; Q65780, GAE1_CYATE; Q43070, GAE1_PEA; Q9SN58, GAE2_ARATH; Q65781, GAE2_CYATE; Q910A7, GAE3_ARATH; Q9KDV3, GALE_BACHD; P55180, GALE_BACSU; P33119, GALE_CORDI; Q45291, GALE_CORGL; Q9WDF5, GALE_DROME; P09147, GALE_ECOLI; P35673, GALE_ERWAM; P24325, GALE_HAEIN; Q14376, GALE_HUMAN; P45602, GALE_KLEPN; Q84903, GALE_IACCA; Q57664, GALE_METJA; P47364, GALE_MYCGE; P75517, GALE_MYCPN; Q05026, GALE_NEIGO; P56997, GALE_NEIMA; P56985, GALE_NEIMB; P56986, GALE_NEIMC; Q59678, GALE_PASHA; Q9CNY5, GALE_PASMU; P18643, GALE_RAT; Q56093, GALE_SALT1; P22715, GALE_SALTY; P13226, GALE_STRLI; P96995, GALE_STRMU; P21977, GALE_STRTR; Q56623, GALE_VIBCH; Q57301, GALE_YEREN; Q9F7D4, GALE_YERPE; P56600, GALX_CANMA; P09609, GALX_KLULA; P40801, GALX_PACTA; Q9H DU3, GALX_SCHPO; P04397, GALX_YEAST;

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[\[General\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

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General information about the entry

Entry name **GALE_ECOLI**
Primary accession number **P09147**
Secondary accession numbers **None**
Entered in Swiss-Prot in **Release 10, March 1989**
Sequence was last modified in **Release 10, March 1989**
Annotations were last modified in **Release 41, February 2003**
Name and origin of the protein
Protein name **UDP-glucose 4-epimerase**
Synonyms **EC 5.1.3.2
Galactowaldenase
UDP-galactose 4-epimerase**
Gene name **GALE or GALD or B0759**
From **Escherichia coli [TaxID: 562]**
Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia**
References

- [1] SEQUENCE FROM NUCLEIC ACID.
MEDLINE=87040735; PubMed=3022232; [NCBI, ExPASy, EBI, Israel, Japan]
Lemaire H.-G., Mueller-Hill B.;
"Nucleotide sequences of the gal E gene and the gal T gene of E. coli.";
Nucleic Acids Res. 14:7705-7711(1986).
- [2] REVISIONS.
Lemaire H.-G.;
Submitted (APR-1988) to the EMBL/GenBank/DDBJ databases.
- [3] SEQUENCE FROM NUCLEIC ACID.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503; [NCBI, ExPASy, EBI, Israel, Japan]
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
- [4] SEQUENCE FROM NUCLEIC ACID.
STRAIN=K12;
MEDLINE=97061202; PubMed=8905232; [NCBI, ExPASy, EBI, Israel, Japan]
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sanpei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
- [5] SEQUENCE OF 1-31 FROM NUCLEIC ACID.
STRAIN=K12;
MEDLINE=96151473; PubMed=8564363; [NCBI, ExPASy, EBI, Israel, Japan]
Walkenhorst H.M., Hemschmeier S.K., Eichenlaub R.;
"Molecular analysis of the molybdate uptake operon, modABCD, of Escherichia coli and modR, a regulatory gene.";
Microbiol. Res. 150:347-361(1995).
- [6] SEQUENCE OF 1-6 FROM NUCLEIC ACID.
MEDLINE=83183658; PubMed=6301942; [NCBI, ExPASy, EBI, Israel, Japan]
Busby S., Oreyfus M.;

"Segment-specific mutagenesis of the regulatory region in the Escherichia coli galactose operon: isolation of mutations reducing the initiation of transcription and translation.";
Gene 21:121-131(1983).

- [7] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
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Bauer A.J., Rayment I., Frey P.A., Holden H.M.;
"The molecular structure of UDP-galactose 4-epimerase from Escherichia coli determined at 2.5-A resolution.";
Proteins 12:372-381(1992).
- [8] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE=96180680; PubMed=8611559; [NCBI, ExPASy, EBI, Israel, Japan]
Thoden J.B., Frey P.A., Holden H.M.;
"Crystal structures of the oxidized and reduced forms of UDP-galactose 4-epimerase isolated from Escherichia coli.";
Biochemistry 35:2557-2566(1996).
- [9] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE=97084800; PubMed=8931134; [NCBI, ExPASy, EBI, Israel, Japan]
Thoden J.B., Frey P.A., Holden H.M.;
"High-resolution X-ray structure of UDP-galactose 4-epimerase complexed with UDP-phenol.";
Protein Sci. 5:2149-2161(1996).
- [10] X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
MEDLINE=97317070; PubMed=9174344; [NCBI, ExPASy, EBI, Israel, Japan]
Thoden J.B., Hegeman A.D., Wesenberg G., Chapeau M.C., Frey P.A., Holden H.M.;
"Structural analysis of UDP-sugar binding to UDP-galactose 4-epimerase from Escherichia coli.";
Biochemistry 36:6294-6304(1997).
- [11] X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF SER-124 MUTANTS.
MEDLINE=97419132; PubMed=9271499; [NCBI, ExPASy, EBI, Israel, Japan]
Thoden J.B., Gulick A.M., Holden H.M.;
"Molecular structures of the S124A, S124T, and S124V site-directed mutants of UDP-galactose 4-epimerase from Escherichia coli.";
Biochemistry 36:10685-10695(1997).
- [12] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANTS.
MEDLINE=98376428; PubMed=9708982; [NCBI, ExPASy, EBI, Israel, Japan]
Thoden J.B., Holden H.M.;
"Dramatic differences in the binding of UDP-galactose and UDP-glucose to UDP-galactose 4-epimerase from Escherichia coli.";
Biochemistry 37:11469-11477(1998).

Comments

- **CATALYTIC ACTIVITY:** UDP-glucose = UDP-galactose.
- **COFACTOR:** NAD.
- **PATHWAY:** Galactose metabolism; third step.
- **SUBUNIT:** Homodimer.
- **SIMILARITY:** BELONGS TO THE SUGAR EPIMERASE FAMILY.

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Cross-references

EMBL	X06226; CAA29573.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE000178; AAC73846.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	D90714; BAA35421.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	U07867; AAB06890.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	J01613; AAA87978.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	S02089; XUECUG.
	2UDP; 18-MAR-98. [ExPASy / RCSB]
	1NAH; 23-DEC-96. [ExPASy / RCSB]
	1NAI; 23-DEC-96. [ExPASy / RCSB]
	1XEL; 12-FEB-97. [ExPASy / RCSB]
PDB	1UDA; 14-JAN-98. [ExPASy / RCSB]
	1UDB; 14-JAN-98. [ExPASy / RCSB]
	1UDC; 14-JAN-98. [ExPASy / RCSB]
	1KVQ; 17-JUN-98. [ExPASy / RCSB]
	1KVR; 18-MAR-98. [ExPASy / RCSB]
	1KVS; 18-MAR-98. [ExPASy / RCSB]
	1KVT; 18-MAR-98. [ExPASy / RCSB]
	1KVU; 18-MAR-98. [ExPASy / RCSB]

1A9Y; 25-NOV-98. [ExPASy / RCSB]
 1A9Z; 25-NOV-98. [ExPASy / RCSB]
 Detailed list of linked structures.
 EcoGene EG10362; galE.
 EcoCyc EG10362; galE.
 CMR P09147; B0759.
 InterPro IPR001509; Epimerase_Dh.
 IPR005886; GalE.
 Graphical view of domain structure.
 Pfam PF01370; Epimerase; 1.
 TIGRFAMs TIGR01179; galE; 1.
 ProDom [Domain structure / List of seq. sharing at least 1 domain].
 BLOCKS P09147.
 ProtoNet P09147.
 ProtoMap P09147.
 PRESAGE P09147.
 DIP P09147.
 ModBase P09147.
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Keywords

Isomerase; NAD; Galactose metabolism; 3D-structure; Complete proteome.

Features



Feature table viewer

Key	From	To	Length	Description
NP_BIND	2	33	32	NAD (POTENTIAL).
STRAND	2	6	5	
TURN	7	9	3	
HELIX	11	22	12	
TURN	23	24	2	
STRAND	26	31	6	
TURN	38	39	2	
HELIX	40	48	9	
TURN	49	49	1	
STRAND	53	56	4	
TURN	59	60	2	
HELIX	62	71	10	
TURN	72	73	2	
STRAND	76	79	4	
HELIX	86	91	6	
HELIX	93	114	22	
TURN	115	115	1	
STRAND	118	124	7	
HELIX	125	128	4	
STRAND	136	136	1	
TURN	138	139	2	
HELIX	148	166	19	
TURN	168	169	2	
STRAND	171	177	7	
STRAND	179	181	3	
TURN	185	186	2	
HELIX	200	208	9	
TURN	209	210	2	
STRAND	215	218	4	
STRAND	230	231	2	
STRAND	233	235	3	
HELIX	236	250	15	

TURN	251	252	2
STRAND	255	261	7
STRAND	267	268	2
HELIX	269	280	12
TURN	281	281	1
STRAND	286	289	4
TURN	293	294	2
STRAND	298	298	1
STRAND	301	301	1
HELIX	304	310	7
HELIX	318	331	14
TURN	333	334	2

Sequence information

Length: 338 AA Molecular weight: 37265 Da CRC64: 5CA8B4F7903F7792 [This is a checksum on the sequence]

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MRVLVTGGSG	YIGSHTCVQL	LQNGHDVIL	DNLCNSKRSV	LPVIERLGK	HPTFVEGDIR
70	80	90	100	110	120
NEALMTEILM	DHAIDTVIHF	AGLKAVGESV	CKPLEYYDNN	VNGTLRLISA	MRAANVKNEI
130	140	150	160	170	180
FSSSATVYGD	QPKIPYVESF	PTGTPQSPYG	KSKLMVEQIL	TDLQKAQPDW	SIALLRYPNP
190	200	210	220	230	240
VGAHPSGDMG	EDPQGIPIINL	MPYIAQVAVG	FRDSIAIFGN	DYPTEDGTGV	RDYIHVMDLA
250	260	270	280	290	300
DGHVVAMEKL	ANKPGVHIYN	LGAGVGNVSL	DVVNAFSKAC	GKPVNYHEAP	RREGDLPAYW
310	320	330			
ADASKADREL	NWRVTRILDE	MAQDTWHWQS	RHPQGYPD		

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[PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)



[ScanProsite](#), [MotifScan](#)



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Hosted by NCSC US Mirror sites: Canada China Korea Switzerland Taiwan				
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General information about the entry

Entry name **GAL7_ECOLI**
Primary accession number **P09148**
Secondary accession number **P78270**
Entered in Swiss-Prot in **Release 10, March 1989**
Sequence was last modified in **Release 35, November 1997**
Annotations were last modified in **Release 42, September 2003**
Name and origin of the protein
Protein name **Galactose-1-phosphate uridylyltransferase**
Synonyms **EC 2.7.7.12**
Gal-1-P uridylyltransferase
UDP-glucose-hexose-1-phosphate uridylyltransferase
Gene name **GALT or GALB or B0758**
From **Escherichia coli [TaxID: 562]**
Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.**

References

- [1] SEQUENCE FROM NUCLEIC ACID.
MEDLINE=87040735; PubMed=3022232; [NCBI, ExPASy, EBI, Israel, Japan]
[Lemaire H.-G., Mueller-Hill B.;](#)
"Nucleotide sequences of the gal E gene and the gal T gene of E. coli.";
[Nucleic Acids Res. 14:7705-7711\(1986\).](#)
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503; [NCBI, ExPASy, EBI, Israel, Japan]
[Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.E., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;](#)
"The complete genome sequence of Escherichia coli K-12.";
[Science 277:1453-1474\(1997\).](#)
- [3] SEQUENCE FROM NUCLEIC ACID.
STRAIN=K12;
MEDLINE=97061202; PubMed=8905232; [NCBI, ExPASy, EBI, Israel, Japan]
[Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;](#)
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";

DNA Res. 3:137-155(1996).

[4] SEQUENCE OF 294-348 FROM NUCLEIC ACID.

MEDLINE=85215584; PubMed=3158881; [NCBI, ExPASy, EBI, Israel, Japan]

Debouck C., Riccio A., Schumperli D., McKerney K., Jeffers J., Hughes C., Rosenberg M., Heusterspreute M., Brunel F., Davison J.;

"Structure of the galactokinase gene of Escherichia coli, the last (?) gene of the gal operon.";

Nucleic Acids Res. 13:1841-1853(1985).

[5] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

MEDLINE=95399389; PubMed=7669762; [NCBI, ExPASy, EBI, Israel, Japan]

Wedekind J.E., Frey P.A., Rayment I.;

"Three-dimensional structure of galactose-1-phosphate uridylyltransferase from Escherichia coli at 1.8-A resolution.";

Biochemistry 34:11049-11061(1995).

[6] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

MEDLINE=97178806; PubMed=9063869; [NCBI, ExPASy, EBI, Israel, Japan]

Thoden J.B., Ruzicka F.J., Frey P.A., Rayment I., Holden H.M.;

"Structural analysis of the H166G site-directed mutant of galactose-1-phosphate uridylyltransferase complexed with either UDP-glucose or UDP-galactose: detailed description of the nucleotide sugar binding site.";

Biochemistry 36:1212-1222(1997).

Comments

- **CATALYTIC ACTIVITY:** UDP-glucose + alpha-D-galactose 1-phosphate = alpha-D-glucose 1-phosphate + UDP-galactose.
- **COFACTOR:** Binds 1 zinc and 1 iron ion per subunit.
- **PATHWAY:** Galactose metabolism; second step.
- **SUBUNIT:** Homodimer.
- **SIMILARITY:** Belongs to the galactose-1-phosphate uridylyltransferase family 1.

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Cross-references

EMBL	X06226; CAA29574.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE000178; AAC73845.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	D90714; BAA35420.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	X02306; CAA26171.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	S00722; XNECUD.
PDB	1GUP; 12-NOV-97. [ExPASy / RCSB]
	1GUQ; 12-NOV-97. [ExPASy / RCSB]
	1HXP; 08-NOV-96. [ExPASy / RCSB]
	1HXQ; 22-OCT-97. [ExPASy / RCSB]
	<u>Detailed list of linked structures.</u>
EcoGene	EG10366; galT.
EcoCyc	EG10366; galT.
CMR	P09148; B0758.
InterPro	IPR001937; GalP_UDPtransf1.
	IPR005851; GalP_Utransf_1.
	IPR005850; GalP_Utransf_C.
	IPR005849; GalP_Utransf_N.
	<u>Graphical view of domain structure.</u>
Pfam	PF02744; GalP_UDP_tr_C; 1.
	PF01087; GalP_UDP_transf; 1.

ProDom PD005051; GalP_UDPtransf1; 1.
[Domain structure / List of seq. sharing at least 1 domain]
TIGRFAMs TIGR00209; galT_1; 1.
PROSITE PS00117; GAL_P_UDP_TRANSF_I; 1.
HOBACGEN [Family / Alignment / Tree]
BLOCKS P09148.
ProtoNet P09148.
ProtoMap P09148.
PRESAGE P09148.
DIP P09148.
ModBase P09148.
SWISS-2DPAGE Get region on 2D PAGE.

Keywords

Transferase; Zinc; Iron; Metal-binding; Nucleotidyltransferase; Galactose metabolism; 3D-structure;
Complete proteome.

Features



Feature table viewer

Key	From	To	Length	Description
ACT_SITE	166	166		NUCLEOPHILE.
METAL	52	52		ZINC.
METAL	55	55		ZINC.
METAL	115	115		ZINC.
METAL	164	164		ZINC.
METAL	182	182		IRON.
METAL	281	281		IRON.
METAL	296	296		IRON.
METAL	298	298		IRON.
CONFLICT	29	31		AKR -> LS (IN REF. 1).
TURN	6	8	3	
STRAND	11	15	5	
TURN	16	19	4	
STRAND	20	24	5	
TURN	26	27	2	
HELIX	28	30	3	
TURN	50	51	2	
TURN	53	54	2	
TURN	56	57	2	
STRAND	59	59	1	
TURN	61	62	2	
STRAND	65	65	1	
STRAND	73	76	4	
TURN	78	79	2	
TURN	84	85	2	
STRAND	99	101	3	
STRAND	104	110	7	
TURN	115	116	2	
HELIX	119	121	3	

HELIX	124	144	21
STRAND	147	154	8
HELIX	156	158	3
TURN	159	159	1
STRAND	166	172	7
HELIX	177	193	17
HELIX	197	208	12
TURN	210	211	2
STRAND	212	215	4
STRAND	219	222	4
TURN	225	226	2
TURN	230	231	2
STRAND	233	237	5
HELIX	244	246	3
HELIX	249	270	22
TURN	271	271	1
STRAND	276	281	6
TURN	291	292	2
STRAND	296	300	5
STRAND	303	306	4
TURN	307	308	2
STRAND	309	310	2
HELIX	315	319	5
TURN	320	320	1
STRAND	323	324	2
HELIX	328	336	9
TURN	337	337	1
HELIX	343	346	4

Sequence information

Length: 348 AA Molecular weight: 39645 Da CRC64: 3D55D2CB38D8C9A2 [This is a checksum on the sequence]

10	20	30	40	50	60
MTQFNPDHP	HRRYNPLTGQ	WILVSPHRAK	RPWQGAQETP	AKQVLPADHP	DCFLCAGNVR
70	80	90	100	110	120
VFGDKNPDYT	GTIVFTNDEA	ALMSDTPDAP	ESHDPMLRCQ	SARGTSRVIC	FSPDHSKTLF
130	140	150	160	170	180
ELSVAALTEI	VKTWQEQTAE	LGKTPWVQV	FENKGAAMGC	SNPHPHGQIW	ANSFLPNEAE
190	200	210	220	230	240
REDRLQKEYF	AEQKSPMLVD	YVQRELADGS	RTVVETEHL	AVVPYWAAMP	FETLLLPKAE
250	260	270	280	290	300
VLRTDLTDA	QRSDLALALK	KLTSRYDNLF	QCSFPYSMGW	HGAPFNGEEN	QHWQLHAHFI
310	320	330	340		
DPLLRSATVR	KFMVGYEMLA	ETQDLTAEQ	AAERLRAVSD	INFRESGV	

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[pI/Mw](#), [PeptideMass](#), [PeptideCutter](#), [Dotlet](#) (Java)



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